BLAST Basic Local Alignment Search Tool

-

Blast 2 sequences

X98077:Higashi-X4

Results for: [emb|X98077.1 Hepatitis B virus complete genome, wild type(3215bp)] ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
   gi|1914699|emb|X98077.1|HBVCGWITY
Description
   Hepatitis B virus complete genome, wild type
Molecule type
   nucleic acid
Query Length
   3215

Subject ID
   14437
Description
   None
Molecule type
   nucleic acid
Subject Length
   23
Program
   BLASTN 2.2.20+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

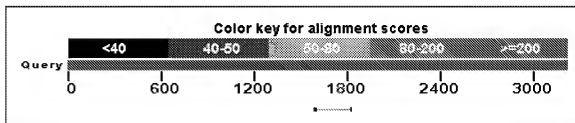| Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 41665

Graphic Summary

Distribution of 2 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

| 0 | 600 | 1200 | 1800 | 2400 | 3000 |

Dot Matrix View

Plot of gi|1914699|emb|X98077.1|HBVCGWITY vs 14437 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: U UniGene E GEO G Gene Structure M Map Viewer

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Sequences producing significant alignments:
(Click headers to sort columns)
14437                                              42.8   63.9   1%   6e-09 100%
```

Alignments Select All Get selected sequences Distance tree of results

>lcl|14437
Length=23

 Score = 42.8 bits (46), Expect = 6e-09
 Identities = 23/23 (100%), Gaps = 0/23 (0%)
 Strand=Plus/Minus

Query 1588   GCTTCACCTCTGCACGTCGCATG   1610
              |||||||||||||||||||||||
Sbjct 23   GCTTCACCTCTGCACGTCGCATG   1

 Score = 21.1 bits (22), Expect = 0.018
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 1824   TTCACCTCTGC   1834
              |||||||||||
Sbjct 21   TTCACCTCTGC   11

Select All Get selected sequences Distance tree of results